How Fast can Virtual Amoebae Aggregate? Analysis for the Optimal Firing Rate in an Instance of the Reaction-Diffusion-Chemotaxis Aggregation Scheme

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Abstract

Decentralised gathering is a challenging problem in systems involving numerous identical agents. In our current work we analyse the dynamics of a gathering model that is based on *virtual amoebae* that fire reaction-diffusion waves with a given probability. Interestingly, it has been shown that there exists a tuning of this probability that minimises the aggregation time. Our study is aimed at experimentally measuring this optimal value and analysing how it is related to the dynamics of the model.

1 Introduction

The reaction-diffusion-chemotaxis aggregation scheme was introduced as a solution to the decentralised gathering problem. Informally, this problem considers the case where identical agents are randomly initially distributed on a lattice and have to group to form a compact cluster. Each agent is not aware of its position, neither aware of the presence or positions of the other agents. Assume that there is no direct communication among the agents, and they can only interact with each other by exchanging messages that are transferred by the environment. Further, each agent interacts with the environment by either initiating the transmission of a message, that we call *firing*, or by reacting to the presence of a message in its neighbourhood by means of *chemotaxis*.

This aggregation scheme draws its inspiration from the species *Dictyostelium discoideum*. This particular species of amoebae has a very diverse life-cycle, and is known for exhibiting a rich variety of properties, such as cell differentiation, chemotaxis, grouping into a single organism, etc. Starting from single individuals that consume the resources of their environment, they form a single multi-cellular organism when the resources are depleted. This organism moves

collectively until a new area that is rich in resources is found and releases spores that start a new life-cycle. During that life period, each amoeba releases a chemical agent that is diffused into the environment and attracts nearby agents by means of chemotaxis. After releasing the chemical agent, each amoeba becomes refractory and insensitive for a period of time. Following that, a new cycle of accumulation and release of the chemical agent follows. The properties of *Dictyostelium discoideum* have been extensively studied, and several models have been developed, either trying to imitate or model its behaviour, see for example [Nag00], [TBW97], [Aga94].

We here study an instance of the reaction-diffusion-chemotaxis aggregation scheme that we call the *virtual amoebae model*, or amoebae model, for short. The amoebae model has been introduced in [Fat10]. It is formed by a two-layered cellular automaton, with one layer corresponding to the environment while the second layer models the amoebae. In the first layer the transmission of the chemical agents is simulated by using a simple reaction-diffusion cellular automaton, see [GHH78], [Wei97]. In the second layer the movements of the amoebae are guided by presence of chemical agents in the first layer, that we call *chemotaxis*. The "coupling" of the agent layer with the environment layer is achieved by letting each agent to initiate the transmission of the chemical agent, that we call *firing*. The firing events of each amoeba occur randomly. The *firing probability* of each agent is constant over time and is denoted by λ.

This current study is mainly focused on identifying an optimal firing probability, λ^*, that minimises the aggregation time. Finding this probability is important both in the merit of applications as well as controlling the behaviour of the model. The existence of an optimal firing probability has first been observed in [Fat10], but was not studied further. Our purpose here is to give an experimental study of how λ^* varies with different simulation conditions and show how the existence of an optimal value is related to the presence of two qualitatively different behaviours of the model.

The paper is organised as follows: In the next section, we describe shortly the basic characteristics of the model, its parameters and we outline the observed model behaviour. Following that, Sec. 3 describes the experimental procedure that we used to determine the optimal firing rate, as well as our observations and comments on the dynamical behaviour of the system. Finally, Sec. 4 presents our conclusions and future studies.

2 Model Description

As we mentioned above , the *amoebae* model consists of two different layers on a cellular automaton, one that models the environment and one that models the behaviour of the amoebae. These two layers are coupled, so that the state of the the environment is affected by the amoebae and the amoebae react to changes in the environment. More specifically, chemical agent transmission is modelled using the Greenberg-Hastings reaction-diffusion model, [GHH78].

2.1 Environment Layer

Let $\mathcal{L} = \{1, \ldots, L\} \times \{1, \ldots, L\}$ be a square array of cells, where L is the environment size. At time t with each cell $c = (c_x, c_y)$ is associated a state σ_c^t, such that $\sigma_c^t \in \{M, \ldots, 0\}$. State M is called the *excited* state, state 0 the *neutral* state, while states $M-1, \ldots, 1$ are the *refractory* states. Each cell c is connected to its 8 nearest neighbours $\mathcal{N}_c$ according to

$$\mathcal{N}_c \quad = \quad \{c' \in \mathcal{L} : \max(|c_x - c'_x|, |c_y - c'_y|) = 1\}$$

The time evolution of the state each cell can be described as a function of its current state σ_c^t and the states of the cells in $\mathcal{N}_c$. Let E_c^t denote the number of excited cells in the neighbourhood of c at time t, $E_c^t = \{c' \in \mathcal{N}_c : \sigma_{c'}^t = M\}$. Then,

$$\sigma_c^t \quad = \quad \begin{cases} M, & \sigma_c^t = 0 \text{ and } |E_c| > 0 \\ \sigma_c^t - 1, & \sigma_c^t \in \{1, \ldots, M-1\} \\ 0, & \text{otherwise} \end{cases}$$

Note that other neighbourhood types are also possible, as for example 4-connected neighbourhood, circular, hexagonal, and so on. Different instances of the amoebae model with different topologies were tested in [Fat10] and it has been shown that aggregation is successful in all cases. Also note that the environment we use has *free* boundaries so that the reaction-diffusion waves that reach the boundary cells are absorbed.

2.2 Amoebae Layer

From the cellular automata viewpoint, the amoebae are represented in the environment as a property of the cells, in addition to the cell state. Let P_c^t denote the number of amoebae that are located at time t in cell c. Since we don't assume any death or birth process, the number of amoebae is constant, $\sum_{c \in \mathcal{L}} P_c^t = \text{const}$. A cell will be called *empty* if it contains no amoebae and *free* if it contains less than two amoebae. An amoeba can only move to a free cell. If a cell contains more than one amoebae, only one of them will move at each time. This approach simplifies the conflict solving procedure in each cell that would be required to impose a limit on the number of amoebae that a cell may contain. The motion of amoebae is governed by the following rules:

- Move randomly to a free *excited* neighbouring cell.
- Otherwise, stay on the same cell.

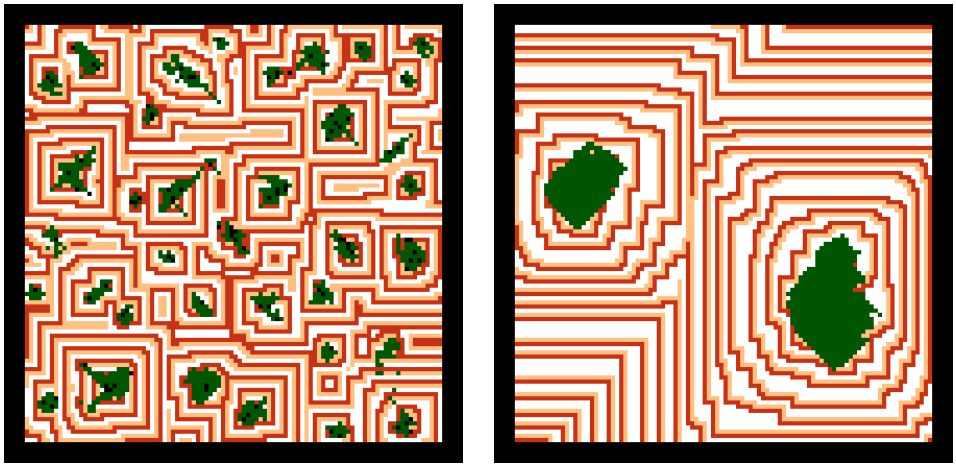
An alternative, equivalent, view of the amoebae model would be that of a multi-agent system, in which the agents "reside" on a two-dimensional grid. The main difference between these two perspectives is that the former is more suitable for computational purposes, since the existence and number of amoebae in each cell can either be incorporated into the cell state or included as a secondary cell state, while the latter focuses on the system as interacting agents. This duality is further discussed in [SFS09].

2.3 Coupling

The coupling of the two layers defines how the amoebae interact with the environment and how chemotaxis is accomplished. This interaction is described by the following informal rules.

- At each time step, an amoeba that is on a neutral cell initiates the transmission of a reaction-diffusion wave with probability λ.
- If an amoeba that lies on a neutral cell detects excited cells in its neighbourhood, it moves towards one randomly selected excited cell.

Movements of the amoebae happen when a reaction-diffusion wavefront has reached their neighbourhood. Although the above rules are very simple, the process of aggregation has been shown, in the previous study, to be robust to the presence of obstacles in the environment and noise on the movements of the amoebae. For a more thorough description of these properties, see [Fat10].



(a) (b)

Figure 1: Snapshots of simulations for $\lambda = 0.6, d_{\mathrm{A}} = 0.15, L = 100$ (a) Small cluster formation during the first phase of aggregation ($t = 500$) (b) An example of two competing clusters, obtained for $t \sim 4000$

2.4 Qualitative Description of Model Characteristics

We now discuss qualitatively what is the expected and observed model behaviour with respect to the probability of transmission, λ. First of all, note that as λ tends to 0 then the probability that a wave is fired will tend to 0 as well, so the time required for the aggregation will grow and for $\lambda = 0$ it is infinite. Similarly, as λ tends to 1, the amoebae will transmit with a very high probability

at each time step. Since reaction-diffusion waves annihilate as they collide, the probability that a reaction-diffusion wave will reach an amoeba, depends on the probability that the amoeba will not fire a wave, $1 - \lambda$, and therefore will decrease as $\lambda \to 1$. For $\lambda = 1$ all amoebae will fire at the maximum rate and no chemotaxis will take place, since no waves will ever reach an amoeba, which results in an infinite aggregation time.

Since the time required for the agents to form a single cluster tends to infinity as $\lambda \to 0$ or $\lambda \to 1$ we expect that there exists at least one value of λ that minimises the time required for the agents to aggregate.

3 Experimental Results

3.1 Experimental Protocol

We determine the time required for the agents to aggregate by measuring the number of different clusters at each time step. Formally, using notions from graph theory, we may define a cluster as follows. Let $G = \{c_1, \ldots, c_N\}$ denote the set of cells c such that $P_c^t > 0$. Define $C^+ = \{c \in \mathcal{L} : P_c^t > 0\}$. Further, for $i \in \mathcal{L}$ let $\Gamma(\{i\}) = \{j \in \mathcal{L} : j \in \mathcal{N}_i \cap C^+\}$ and for $I \subset \mathcal{L}$, $\Gamma(I) = \cup_{i \in I} \Gamma(i)$. Using the latter, define $\Gamma^2(i) = \Gamma(\Gamma(i))$ and similarly $\Gamma^*(i) = \Gamma(\Gamma(\ldots \Gamma(i) \ldots))$, the transitive closure of the graph defined on agents and the edge relation defined by Γ. The number of connected components can be expressed compactly as $|\{\Gamma^*(i) : i \in \mathcal{L}\}|$. Determining the formation of a single cluster is accomplished by counting the number of connected components of the graph generated this way. This is equivalent to assigning to each group of amoebae that belong to the same connected component a "colour" property and then counting the number of different "colours". The algorithm we used was based on a recursive exploration and "colouring" of the neighbourhood of each amoeba. Let n_{C} denote the number of colours and $\mathrm{col}(c)$ the colour property.

▷ procedure *recursivePaint(c, col)*

  ▷ col(c) ← col

    $\forall c' \in \mathcal{N}_c : \mathrm{col}(c) = 0$ and $P_{c'} > 0$

      recursivePaint(c′, col)

  end procedure

• // main procedure

▷ $n_{\mathrm{C}} \leftarrow 0$

▷ $\forall c \in L,\ \mathrm{col}(c) \leftarrow 0$

▷ $\forall c \in L$

If $P_c > 0$ and $\mathrm{col}(c) = 0$

$n_\mathrm{C} \leftarrow n_\mathrm{C} + 1,\ \mathrm{col}(c) \leftarrow n_\mathrm{C}$

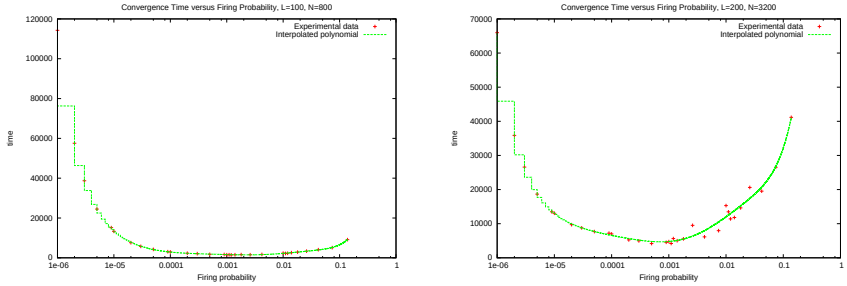
recursivePaint(c, n_C)

$\triangleright$ return n_C

If there is only one colour, then the aggregation of the amoebae into a single cluster has been completed.

Each experiment can be defined by the following set of parameters: the grid dimension L, the number of amoebae N and their initial distribution, the firing probability λ as well as the neighbourhood type $\mathcal{N}_c$ and the number of states of the reaction diffusion waves, M. To identify the dependence $\lambda^* = f(N, L)$ we measure the aggregation time by repeating N_S times the simulations. For the sake of simplicity, we do not examine the dependence on M and fix $M = 4$ in all the experiments.

Figure 2 depicts an example of the results of our experiments for a constant density and two different environment sizes[1]. The curves clearly show the existence of an optimal firing probability. To identify λ^* from the mean measured aggregation times for each L and N, we used the following method: Starting from a polynomial of small degree, we did a numerical polynomial fit on $t(\log(\lambda))$, and by inspecting the resulting curves, we progressively increased the number of factors, taking care not to obtain an "over-fitted" polynomial. Then, by differentiating the resulting polynomial, we identified the value $\log(\lambda))$ where the derivative changed sign and that corresponded to a minimum number of time steps required for convergence.



$L = 100, N = 800, d_\mathrm{A} = 0.08$ $\quad$ $L = 200, N = 3200, d_\mathrm{A} = 0.08$

Figure 2: Examples of convergence time versus λ plots, where the interpolated polynomial is also shown

The experimental values covered three grid sizes, $L = 100, 150, 200$ and number of amoebae that corresponds to densities d_A ranging from 0.01 to 0.43 with a step 0.07. The value of λ ranged from 0.00001 to 0.16. We used $N_\mathrm{S} = 30$

[1] see `http://www.loria.fr/~fates/Amybia/project.html` for the remaining curves that we used to obtain our results on λ^*

samples per experiment, as the major limiting factor for the quality of our result was the time required to perform the simulations.

Figure 3 shows the dependency of λ^* on L and N (or d_{A}). As we observe, the points for the three different grid sizes seem to follow similar laws, and decrease rapidly as the density increases.

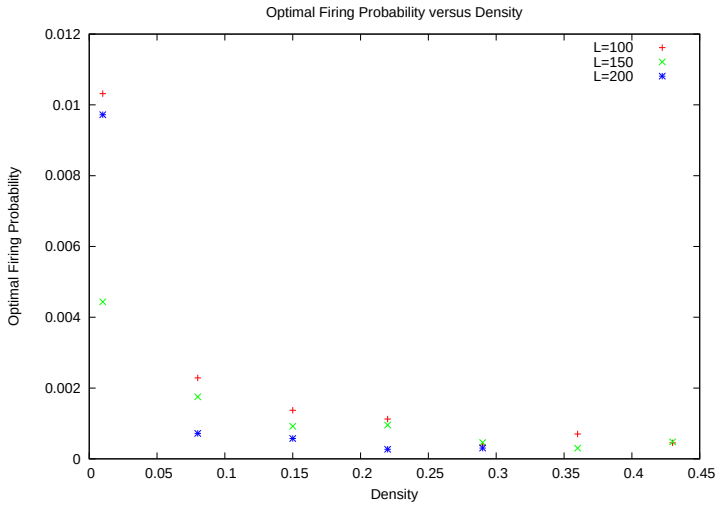


Figure 3: Plot of λ^* versus time for the different environment sizes.

3.2 Interpretation of the Results

To better understand the results, we propose to define the following qualitative phases during the aggregation process.

1 Immediately after the initialisation of an experiment, and for relatively high values of λ the amoebae form small condensates, as is shown in Fig. 1.a.

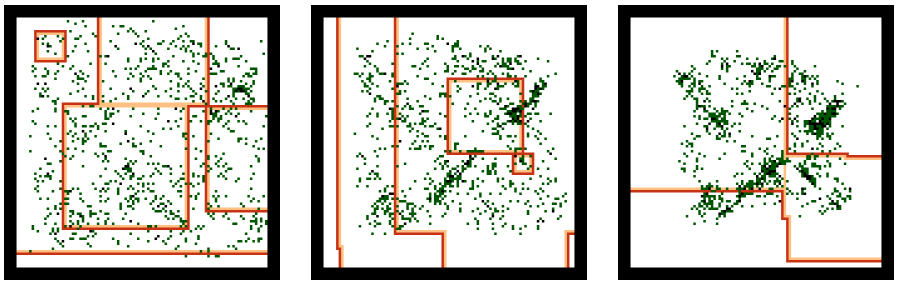
2 During the second phase, the local condensates are progressively merged into larger size groups

3 The last phase of aggregation, usually involves few large scale groups of amoebae, that compete among each other, Fig. 1.b. Aggregation completes as soon as one cluster grows significantly in size with respect to the others.

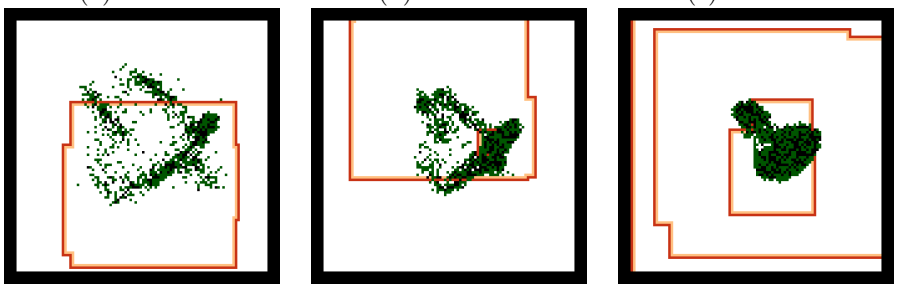
4 A single cluster is formed.

Figures 4 and 5 show the time evolution of the agent aggregation for two different values of λ. We observe on Fig. 4 that that the amoebae converge directly into

a single cluster and that do not go through the phases 1 to 3. In fact, in many cases, for small values of λ the aggregation does not even go through the first phase where the formation of *micro clusters* occurs, and the amoebae converge rapidly to a single cluster. Values of λ much smaller than λ^* display the same behaviour, but with an increased convergence time, since the firing rate is decreased. On the other hand and for relatively high values of λ the system will undergo through phases 1 to 3, as can be seen in Fig. 5. More specifically, as the value of λ increases these phases are further separated into sub-phases, where the initial micro clusters are merged into medium size clusters, and so on, until two or three competing clusters remain. In short, the major factor that slows down the aggregation is the formation of two or more *competing* clusters of amoebae, of similar size. An example of such a formation can be seen in Fig. 1.b. These structures tend to persist for a comparatively large amount of time and usually appear after the first phase, as smaller clusters merge together. As a conclusion, λ^* separates the two qualitative behaviours described above as it corresponds to the highest value of λ for which no competing clusters appear.



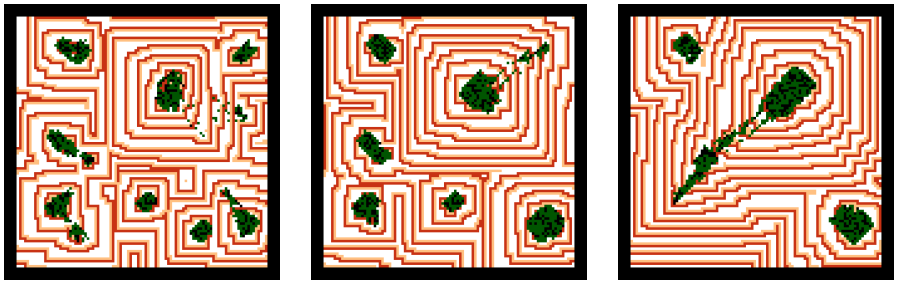
(a) $t = 500$ (b) $t = 1000$ (c) $t = 1500$



(d) $t = 2000$ (e) $t = 2500$ (f) $t = 3000$

Figure 4: Example of the evolution of the aggregation for $\lambda = 0.00001$, $d_{\mathrm{A}} = 0.1$

Now, the dependence of λ^* with respect to the density, seems to follow an inverse proportionality law. To intuitively explain this behaviour, we should mention that as the density increases, the number of events, for constant λ, also increases. To minimise the probability of cluster formation, the firing rate should decrease proportionally, so as to prevent local aggregation to micro clusters that



(a) $t = 500$ (b) $t = 1000$ (c) $t = 2000$

(d) $t = 2500$ (e) $t = 3500$ (f) $t = 4000$

Figure 5: Example of the evolution of the aggregation for $\lambda = 0.08$, $d_{\mathrm{A}} = 0.1$

may subsequently merge into competing clusters.

4 Conclusions and Future Research

The studies of the optimal firing probability gave rise to a series of interesting questions regarding the dynamics and details of the time evolution of the model. An interesting problem is to study to which extent our observations can interpreted as a "symmetry breaking" on the interactions of the agents. This symmetry breaking appears as a change of behaviour in the model, so that, for $\lambda \gg \lambda^*$ the dynamics of the model seem to be governed by the local interactions (small-scale interactions) of agents, that guide the cluster formation, while for $\lambda < \lambda^*$ the model seems to be governed by medium- or large-scale interactions among agents.

On the same subject, studying the dynamics of micro cluster formation and the observed coupling of λ and density fluctuations on the small scale dynamics of the model, for $\lambda > \lambda^*$ is an interesting and rich topic on its own.

Another interesting problem of similar nature deals with the probability of formation of competing clusters as λ varies close to λ^*. As we have mentioned, for probability of wave transmission equal to λ^* the probability that competing clusters will form seems to be minimal. It is therefore interesting to study how the probability of competing cluster formation scales with respect to $|\lambda - \lambda^*|$.

To improve on the quality of our results we are planning on transferring the simulation environment to FPGAs and exploit their inherent parallelism. Although this will significantly reduce the time required for each experiment and increase the quality of our results, it introduces new challenges, as for example, determining the number of clusters is a non-trivial problem when studied in the context of two dimensional meshes / arrays of processors.

Finally, we would like to study the dependence of the aggregation time with respect to the topology used. More specifically, we would like to investigate how λ^* varies for the same parameters and different topologies, i.e. 4-connected, hexagonal and so on. To this end, we are also interested in studying how the aggregation would be affected if we moved towards a true "gradient-following" model. As we mentioned in Sec. 2, currently the amoebae follow only wave-fronts, i.e. will move towards a cell, only if the state of the current cell is neutral and a neighbouring cell is excited. Following gradients, i.e. modifying the amoebae so that they move to a neighbouring cell depending on the difference of the state of the cells would enable them to move a longer distances while following a reaction-diffusion wave, and would probably further reduce convergence time.

Our ongoing studies on the model include modelling of the interactions of the agents, and the possibility that the model dynamics can be approximated by a "potential"-like function that describes the interactions of the agents. Finally, we are currently studying the dynamics of clusters. Given a non-zero probability of cluster formation, we are interested in determining how the clusters behave and what governs their aggregation times. On parallel, we are working on an analytic description of the model, that will verify the observed experimental behaviour.

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